Figure 2 is a schematic diagram which shows the construction of plasmid pKNI5' containing a 5'-region of NIa;

Figure 3 is a schematic diagram which shows the construction of plasmid pKNI5IL containing a part of the IL-11 gene and a 5'-region of NIa;

Figure 4 is a schematic diagram which shows primers which were used to prepare the 5'IL DNA fragment, the CIN3 DNA fragment and in which the 3'-terminus of the NIa gene and the 5'-terminus of the IL-11 gene are fused;

Figure 5 is a schematic diagram which shows the fusion of the CIN3 DNA fragment and the 5'IL DNA fragment by PCR;

Figure 6 is a schematic diagram which shows the construction of plasmid pKSUN9;

Figure 7 is a construction enzyme map of pUCKM31-7;

Figure 8 is a comparative diagram of the nucleotide sequences of the 3' terminals in pUCKM31-7 and pcD-31;

Figure 9 is a construction diagram of pSRα31-7;

Figure 10 is a schematic diagram showing the introduction of a histidine hexamer encoding sequence into pUCKM31-7;

Figure 11 is a construction diagram for pMAL31-7;

A1

Figures 12A and 12B are graphs showing the results of the assay of dichlorophenol-indophenol reducing activity; and

Figure 13 is a graph showing the determination of oxidized glutathione reducing activity.--

Pages 99 and 100: replace the paragraph bridging pages 99 and 100 with the following paragraph:

--The next step was to verify that the several specific 60 kDa bands identified in Example 11 are the same as the polypeptide encoded by the insert of pSRα31-7. It was also desired to determine the N-terminal amino acid sequence of this polypeptide. Accordingly, a clone was prepared wherein an extra six His residues were encoded for the C-terminal of the polypeptide before te step codon. Histidine residues have a high affinity for Ni^{2+} and the objective was to express a polypeptide having a histidine hexomer (6 x His), which could be purified using an affinity resin column charged with Ni^{2+}.--

A2

Pages 105 and 106: replace the paragraph bridging pages 105 and 106 with the following paragraph:

--90.4 µg, as determined using the Protein Assay Kit (Bio-Rad), of each of the chromatography samples obtained in ii) above were separately mixed with 1 ml of 50 µM DCIP (Sigma). 15 µl of 1 mM NADPH (Boehringer-Mannheim) were then added to each of the samples and the OD_{600nm} and OD_{340nm} absorbance values were monitored with time. The resulting decrease in absorbance at both wavelengths is shown in Figures 12A and 12B and it can be seen that only the pMAL31-7 sample contains a factor that reduces DCIP.--

A3

Replace **Page 115**, last paragraph, with the following paragraph:

--The resulting sediment was suspended in SDS-PAGE sample buffer solution containing 10 µl of 2-mercaptoethanol. Each suspension was heated at 90°C for 2 minutes, and then SDS-PAGE was performed under reducing conditions using a 12.5% gel. Following electrophoresis, the product was transferred from polyacrylamide gel to a nitrocellulose film (BIO-RAD). Western

A4

blotting was performed using the polyclonal anti-KM31-7 antibody described in Example 1, part (a) and the anti-KM31-7 monoclonal antibody was determined to specifically precipitate KM31-7 protein from COS-1/pSRα31-7 serum-free culture supernatant.--

Please replace **Pages 127 to 140** (Sequence Listing) with the replacement pages 127 to 140 of the Sequence Listing attached hereto.

? glutathione reductase?

9001-48-3/RN

IN THE CLAIMS:

48. (Amended) A polypeptide having the sequence consisting essentially of residue numbers 4 to 437 in SEQ ID NO:2.

55. (Amended) A polypeptide which consists essentially of amino acid numbers 1 to 526 of SEQ ID NO: 12, and which catalyzes the reduction of dichloroindophenol and oxidized glutathione.

60. (Amended) A polypeptide having the sequence consisting essentially of -23 to 526 of SEQ ID NO: 12.

61. (Amended) A method for the prophylaxis or treatment of conditions caused by, or related to, oxidative stress, or a